



#4

SEQUENCE LISTING

<110> Saxon, Andrew

<120> FUSION MOLECULES AND METHODS FOR
TREATMENT OF IMMUNE DISEASES

<130> UC067.004A

<140> US 10/000,439

<141> 2001-10-24

<150> US 09/847,208

<151> 2001-05-01

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 696

<212> DNA

<213> Homo sapiens

<400> 1

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aactggtacg tggacggcgt ggaggtgcat aatgttaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctaccgtcc tgcaccagaa ctggatgaat 300
ggaaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 360
atctccaaag ccaaagtgca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgctgctg actccgtcgg ctctctcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
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<210> 2

<211> 330

<212> PRT

<213> Homo sapiens

<400> 2

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Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20          25          30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35          40          45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50          55          60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65          70          75          80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85          90          95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100          105          110
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
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		115					120					125					
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	130						135					140					
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp		
145						150					155				160		
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Val	Lys	Thr	Lys	Pro	Arg	Glu		
					165				170					175			
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Ser	Val	Leu	Thr	Val	Leu			
			180					185					190				
His	Gln	Asn	Trp	Met	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn		
		195					200					205					
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Val		
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Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu		
225					230					235					240		
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr		
			245						250					255			
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn		
		260						265					270				
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Val	Gly	Ser	Phe	Phe		
	275					280						285					
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn		
	290					295					300						
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Gln		
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 <212> PRT
 <213> Homo sapiens

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			20					25					30				
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val		
	35						40					45					
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val		
	50					55					60						
Asp	Gly	Val	Glu	Val	His	Asn	Val	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln		
65					70					75					80		
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln		
			85						90					95			
Asn	Trp	Met	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala		
		100						105					110				
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Val	Gln	Pro		
	115						120					125					
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr		
	130					135					140						
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser		
145					150					155					160		
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr		
			165						170					175			
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Val	Gly	Ser	Phe	Phe	Leu	Tyr		
		180						185					190				
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe		
		195					200					205					

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Gln Gln Arg
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 4
 <211> 1445
 <212> DNA
 <213> Homo sapiens

<400> 4
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 acctgggaca caggctccct caacgggaca actatgacct taccagccac caccctcacg 180
 ctctctggtc actatgccac catcagcttg ctgacctct cgggtgctg ggccaagcag 240
 atgttcacct gccgtgtggc acacactcca tcgtccacag actgggtcga caacaaaacc 300
 ttcagcgtct gctccaggga cttcaccccg cccaccgtga agatcttaca gtcgtcctgc 360
 gacggcgggc ggcacttccc cccgaccatc cagctcctgt gcctcgtctc tgggtacacc 420
 ccagggaacta tcaacatcac ctggctggag gacgggcagg tcatggacgt ggacttgtcc 480
 accgcctcta ccacgcagga gggtagctg gcctccacac aaagcgagct caccctcagc 540
 cagaagcact ggctgtcaga ccgcacctac acctgccagg tcacctatca aggtcacacc 600
 tttgaggaca gcaccaagaa gtgtgcagat tccaaccga gaggggtgag cgcctaccta 660
 agccggccca gcccggttga cctgttcac cgcaagtgc ccacgatcac ctgtctggtg 720
 gtggacctgg caccagcaa ggggaccgtg aacctgacct ggtcccgggc cagtgggaag 780
 cctgtgaacc actccaccag aaaggaggag aagcagcgca atggcacgtt aaccgtcacg 840
 tccacctgac cgggtgggac ccgagactgg atcgaggggg agacctacca gtgcagggtg 900
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 agctgtgcag tggggaggac tggccagacc ttctgtccac tgttgcaatg accccaggaa 1380
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<210> 5
 <211> 427
 <212> PRT
 <213> Homo sapiens

<400> 5
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 Ile Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu Ala Thr Gly
 20 25 30
 Tyr Phe Pro Glu Pro Val Met Val Thr Trp Asp Thr Gly Ser Leu Asn
 35 40 45
 Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu Ser Gly His
 50 55 60
 Tyr Ala Thr Ile Ser Leu Leu Thr Val Ser Gly Ala Trp Ala Lys Gln
 65 70 75 80
 Met Phe Thr Cys Arg Val Ala His Thr Pro Ser Ser Thr Asp Trp Val
 85 90 95
 Asp Asn Lys Thr Phe Ser Val Cys Ser Arg Asp Phe Thr Pro Pro Thr
 100 105 110
 Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro Pro
 115 120 125
 Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile

130	135	140															
Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser																	
145	150	155															160
Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu																	
	165	170															175
Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys																	
	180	185															190
Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys																	
	195	200															205
Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro Ser																	
	210	215															220
Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu Val																	
225	230	235															240
Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser Arg																	
	245	250															255
Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln																	
	260	265															270
Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg																	
	275	280															285
Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His																	
	290	295															300
Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser Gly Pro Arg																	
305	310	315															320
Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp Pro Gly Ser																	
	325	330															335
Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe Met Pro Glu																	
	340	345															350
Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu Pro Asp Ala																	
	355	360															365
Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly Phe Phe																	
	370	375															380
Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu Gln Lys Asp																	
385	390	395															400
Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro Ser Gln Thr																	
	405	410															415
Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys																	
	420	425															

<210> 6
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 6
 Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly
 1 5 10 15
 Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr
 20 25 30
 Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met
 35 40 45
 Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala
 50 55 60
 Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp
 65 70 75 80
 Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp
 85 90 95
 Ser Thr Lys Lys Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr
 100 105 110
 Leu Ser Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr
 115 120 125

Ile	Thr	Cys	Leu	Val	Val	Asp	Leu	Ala	Pro	Ser	Lys	Gly	Thr	Val	Asn
130						135					140				
Leu	Thr	Trp	Ser	Arg	Ala	Ser	Gly	Lys	Pro	Val	Asn	His	Ser	Thr	Arg
145					150					155					160
Lys	Glu	Glu	Lys	Gln	Arg	Asn	Gly	Thr	Leu	Thr	Val	Thr	Ser	Thr	Leu
				165					170						175
Pro	Val	Gly	Thr	Arg	Asp	Trp	Ile	Glu	Gly	Glu	Thr	Tyr	Gln	Cys	Arg
			180					185					190		
Val	Thr	His	Pro	His	Leu	Pro	Arg	Ala	Leu	Met	Arg	Ser	Thr	Thr	Lys
		195					200					205			
Thr	Ser	Gly	Pro	Arg	Ala	Ala	Pro	Glu	Val	Tyr	Ala	Phe	Ala	Thr	Pro
	210					215					220				
Glu	Trp	Pro	Gly	Ser	Arg	Asp	Lys	Arg	Thr	Leu	Ala	Cys	Leu	Ile	Gln
225					230					235					240
Asn	Phe	Met	Pro	Glu	Asp	Ile	Ser	Val	Gln	Trp	Leu	His	Asn	Glu	Val
				245					250					255	
Gln	Leu	Pro	Asp	Ala	Arg	His	Ser	Thr	Thr	Gln	Pro	Arg	Lys	Thr	Lys
			260					265					270		
Gly	Ser	Gly	Phe	Phe	Val	Phe	Ser	Arg	Leu	Glu	Val	Thr	Arg	Ala	Glu
	275						280					285			
Trp	Glu	Gln	Lys	Asp	Glu	Phe	Ile	Cys	Arg	Ala	Val	His	Glu	Ala	Ala
	290					295					300				
Ser	Pro	Ser	Gln	Thr	Val	Gln	Arg	Ala	Val	Ser	Val	Asn	Pro	Gly	Lys
305					310					315					320

<210> 7
 <211> 569
 <212> PRT
 <213> Unknown

<220>
 <223> Fusion polypeptide comprising a hinge-CH2-CH3
 (IgG1) sequence and a CH2-CH3-CH4 (IgE) sequence

<400> 7

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Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
			20					25					30		
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
	35						40					45			
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
	50					55					60				
Asp	Gly	Val	Glu	Val	His	Asn	Val	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
65					70					75				80	
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
			85						90					95	
Asn	Trp	Met	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
			100					105					110		
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Val	Gln	Pro
		115					120					125			
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
	130					135					140				
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
145					150					155					160
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
			165						170					175	
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Val	Gly	Ser	Phe	Phe	Leu	Tyr
			180					185					190		
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe

<210> 9
<211> 33
<212> DNA
<213> Unknown

<220>
<223> primer sequence

<400> 9
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33

<210> 10
<211> 32
<212> PRT
<213> Arachis hypogaea (peanut)

<220>
<221> UNSURE
<222> 1, 4, 11, 12, 27, 30
<223> Xaa = any amino acid

<400> 10
Xaa Gln Gln Xaa Glu Leu Gln Asp Leu Glu Xaa Xaa Gln Ser Gln Leu
1 5 10 15
Glu Asp Ala Asn Leu Arg Pro Arg Glu Gln Xaa Leu Met Xaa Lys Ile
20 25 30

<210> 11
<211> 32
<212> PRT
<213> Arachis hypogaea (peanut)

<220>
<221> UNSURE
<222> 1, 4, 8, 10, 11, 12, 27, 30
<223> Xaa = any amino acid

<400> 11
Xaa Gln Gln Xaa Glu Leu Gln Xaa Asp Xaa Xaa Xaa Gln Ser Gln Leu
1 5 10 15
Glu Arg Ala Asp Leu Arg Pro Gly Glu Gln Xaa Leu Met Xaa Lys Ile
20 25 30

<210> 12
<211> 171
<212> PRT
<213> Homo sapiens

<400> 12
Met Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu
1 5 10 15
Ala Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg
20 25 30
His Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly
35 40 45
Asp Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro
50 55 60
Ala Arg Thr Ala His Tyr Gly Ser Leu Pro Gln Lys Ser His Gly Arg
65 70 75 80

Thr	Gln	Asp	Glu	Asn	Pro	Val	Val	His	Phe	Phe	Lys	Asn	Ile	Val	Thr
				85					90					95	
Pro	Arg	Thr	Pro	Pro	Pro	Ser	Gln	Gly	Lys	Gly	Arg	Gly	Leu	Ser	Leu
			100					105					110		
Ser	Arg	Phe	Ser	Trp	Gly	Ala	Glu	Gly	Gln	Arg	Pro	Gly	Phe	Gly	Tyr
		115					120					125			
Gly	Gly	Arg	Ala	Ser	Asp	Tyr	Lys	Ser	Ala	His	Lys	Gly	Phe	Lys	Gly
	130					135					140				
Val	Asp	Ala	Gln	Gly	Thr	Leu	Ser	Lys	Ile	Phe	Lys	Leu	Gly	Gly	Arg
145					150					155					160
Asp	Ser	Arg	Ser	Gly	Ser	Pro	Met	Ala	Arg	Arg					
				165					170						

<210> 13
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 13
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 Pro